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  Query Match            89.1%;  Score 1017;  DB 2;  Length 226;
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  Matches  197;  Conservative   15;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 MEPIKNLPRLCRTLGYEFNNIELLIQALTHRSAANKHNERLEFLGDSILSIAISDALYHQ 60
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Db          1 MEPIKNLPRLCRTLSYEFKNIELLTQALTHRSAANKHNERLEFLGDSILSIVISDALYHQ 60

Qy         61 FPKATEGDLSRMRATLVKGDTLTIIAKEFKLGDYLYLGPGELKSGGFRRESILADAVEAI 120
              |||||||||||||||:||||||||:||||||||||||||||||||||||||||||||||
Db         61 FPKATEGDLSRMRATLVRGDTLTIIAQEFKLGDYLYLGPGELKSGGFRRESILADAVEAI 120

Qy        121 IGAVYLDADIEVCRKLLLSWYQERLAEIKPGINQKDPKTILQEYLQGFKKPLPDYQVVAV 180
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Db        121 IGAVYLDSDLEVCRALLLKWYAERLAEIQPGISQKDAKTLLQEHLQGFKKPLPDYQVINI 180

Qy        181 EGEAHDQTFTVECKISELDKVVTGVASSRRKAEQLAAAQVLELLNK 226
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Db        181 EGDAHDQTFTVECRIEDLSQSVIGVASSRRKAEQIAAAQVLELLKK 226
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RESULT 13
RNC_SHEON
ID   RNC_SHEON               Reviewed;         226 AA.
AC   Q8EH81;
DT   21-MAR-2006, integrated into UniProtKB/Swiss-Prot.
DT   01-MAR-2003, sequence version 1.
DT   24-JUL-2007, entry version 26.
DE   Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III) (RNase III).
GN   Name=rnc; OrderedLocusNames=SO_1348;
OS   Shewanella oneidensis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Shewanellaceae; Shewanella.
OX   NCBI_TaxID=70863;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MR-1;
RX   MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA   Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA   Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA   Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA   Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA   White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA   Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA   Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA   Venter J.C., Nealson K.H., Fraser C.M.;
RT   "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT   Shewanella oneidensis.";
RL   Nat. Biotechnol. 20:1118-1123(2002).
CC   -!- FUNCTION: Digests double-stranded RNA. Involved in the processing
CC       of ribosomal RNA precursors and of some mRNAs (By similarity).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC       phosphomonoester.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
CC   -!- SIMILARITY: Contains 1 RNase III domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AE014299; AAN54413.1; -; Genomic_DNA.
DR   HSSP; Q9X0I6; 100W.
DR   GenomeReviews; AE014299_GR; SO_1348.
DR   KEGG; son:SO1348; -.
DR   TIGR; SO_1348; -.
DR   BioCyc; SONE211586:SO1348-MONOMER; -.
DR   GO; GO:0004525; F:ribonuclease III activity; IEA:HAMAP.
DR   GO; GO:0006397; P:mRNA processing; IEA:HAMAP.
DR   GO; GO:0006364; P:rRNA processing; IEA:HAMAP.
DR   HAMAP; MF_00104; -; 1.
DR   InterPro; IPR001159; Ds_RNA_bd.
DR   InterPro; IPR014720; dsRNA-bd-like.
DR   InterPro; IPR000999; RNase_III.
DR   InterPro; IPR011907; RNase_III_bac.
DR   Gene3D; G3DSA:3.30.160.20; dsRNA-bd-like; 1.
DR   Gene3D; G3DSA:1.10.1520.10; RNase_III; 1.
DR   Pfam; PF00035; dsrm; 1.
DR   Pfam; PF00636; Ribonuclease_3; 1.
DR   SMART; SM00358; DSRM; 1.
DR   SMART; SM00535; RIBOc; 1.
DR   TIGRFAMs; TIGR02191; RNaseIII; 1.
DR   PROSITE; PS50137; DS_RBD; 1.
DR   PROSITE; PS00517; RNASE_3_1; 1.
DR   PROSITE; PS50142; RNASE_3_2; 1.
PE   3: Inferred from homology;
KW   Complete proteome; Cytoplasm; Endonuclease; Hydrolase; Nuclease;
KW   RNA-binding.
FT   CHAIN         1    226       Ribonuclease 3.
FT                                /FTId=PRO_0000228579.
FT   DOMAIN        7    129       RNase III.
FT   DOMAIN      156    226       DRBM.
SQ   SEQUENCE   226 AA;  25297 MW;  7772258B8C0C12C5 CRC64;
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Qy          1 MEPIKNLPRLCRTLGYEFNNIELLIQALTHRSAANKHNERLEFLGDSILSIAISDALYHQ 60
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Qy         61 FPKATEGDLSRMRATLVKGDTLTIIAKEFKLGDYLYLGPGELKSGGFRRESILADAVEAI 120
              |||||||||||||||:|||||:||: |||||||:|||||||||||||||||||||||
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Qy        121 IGAVYLDADIEVCRKLLLSWYQERLAEIKPGINQKDPKTILQEYLQGFKKPLPDYQVVAV 180
              |||:|||:|:||||:|||:|| ||||||:||||||| ||:||||||| |||||||: :
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Qy        181 EGEAHDQTFTVECKISELDKVVTGVASSRRKAEQLAAAQVLELLNK 226
              ||:||||||||||:| :| : | ||||||||||:||||||||| |
Db        181 EGDAHDQTFTVECRIDDLSQSVIGVASSRRKAEQIAAAQVLELLKK 226
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